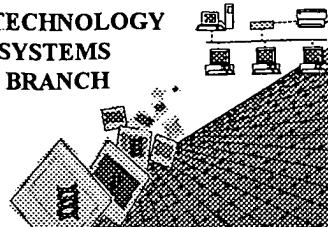


1646

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

#17

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/461,436A
Source: 1600
Date Processed by STIC: 10/18/2002

RECEIVED

OCT 25 2002

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

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OCT 25 2002



TECH CENTER 1600/2900

1600

RAW SEQUENCE LISTING

DATE: 10/18/2002

PATENT APPLICATION: US/09/461,436A

TIME: 13:13:59

Input Set : A:\EP.txt

Output Set: N:\CRF4\10182002\I461436A.raw

SEQUENCE LISTING

Does Not Comply
Corrected Diskette Needed

pp 1-5

OK

(1) GENERAL INFORMATION:

(i) APPLICANT: Shuji Hinuma
Yasuaki Ito
Ryo Fujii

(ii) TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof

(iii) NUMBER OF SEQUENCES: 61

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Edwards & Angell, LLP
(B) P.O. Box 9169
(C) CITY: BOSTON
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02209

STREET: ← insert

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/09/461,436A
(B) FILING DATE: 14-Dec-1999
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/513,974
(B) FILING DATE: 14-SEP-1995
(A) APPLICATION NUMBER: PCT/JP95/01599
(B) FILING DATE: 10-AUG-1995
(A) APPLICATION NUMBER: 7-093989
(B) FILING DATE: 19-APR-1995
(A) APPLICATION NUMBER: 7-057186
(B) FILING DATE: 16-MAR-1995
(A) APPLICATION NUMBER: 7-007177
(B) FILING DATE: 20-JAN-1995
(A) APPLICATION NUMBER: 6-326611
(B) FILING DATE: 28-DEC-1994
(A) APPLICATION NUMBER: 6-270017
(B) FILING DATE: 02-NOV-1994
(A) APPLICATION NUMBER: 6-236357
(B) FILING DATE: 30-SEP-1994
(A) APPLICATION NUMBER: 6-236356
(B) FILING DATE: 30-SEP-1994

do not use TAB
codes; they cause
misalignment.

RAW SEQUENCE LISTING

DATE: 10/18/2002

PATENT APPLICATION: US/09/461,436A

TIME: 13:13:59

Input Set : A:\EP.txt

Output Set: N:\CRF4\10182002\I461436A.raw

63 (A) APPLICATION NUMBER: 6-189274
 64 (B) FILING DATE: 11-AUG-1994
 66 (A) APPLICATION NUMBER: 6-189273
 67 (B) FILING DATE: 11-AUG-1994
 69 (A) APPLICATION NUMBER: 6-189272
 70 (B) FILING DATE: 11-AUG-1994
 C--> 72 (viii) ATTORNEY/AGENT INFORMATION:
 73 (A) NAME: CONLIN, DAVID G.
 C--> 74 (B) REGISTRATION NUMBER:
 75 (C) REFERENCE/DOCKET NUMBER: 45753 DIV2
 77 (ix) TELECOMMUNICATION INFORMATION:
 78 (A) TELEPHONE: 617-439-4444
 79 (B) TELEFAX: 617-439-4170

ERRORED SEQUENCES

563 (2) INFORMATION FOR SEQ ID NO: 26:
 565 (i) SEQUENCE CHARACTERISTICS:
 566 (A) LENGTH: 370
 567 (B) TYPE: Amino acid
 C--> 568 (D) → (D) TOPOLOGY: Linear
 570 (ii) MOLECULE TYPE: Peptide
 572 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
 574 Met Ala Ser Ser Thr Thr Arg Gly Pro Arg Val Ser Asp Leu Phe Ser
 575 1 5 10 15
 577 Gly Leu Pro Pro Ala Val Thr Thr Pro Ala Asn Gln Ser Ala Glu Ala
 578 20 25 30
 580 Ser Ala Gly Asn Gly Ser Val Ala Gly Ala Asp Ala Pro Ala Val Thr
 581 35 40 45
 583 Pro Phe Gln Ser Leu Gln Leu Val His Gln Leu Lys Gly Leu Ile Val
 584 50 55 60
 586 Leu Leu Tyr Ser Val Val Val Val Gly Leu Val Gly Asn Cys Leu
 587 65 70 75 80
 589 Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn
 590 85 90 95
 592 Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
 593 100 105 110

E--> 595 Cys Val Pr
 E--> 598 (1) GENERAL INFORMATION:
 E--> 600 (i) APPLICANT: Shuji Hinuma
 E--> 601 Masaki Hosoya
 E--> 602 Ryo Fujii
 E--> 603 Tetsuya Ohtaki
 E--> 604 Shoji Fukusumi
 E--> 605
 E--> 608 (1) GENERAL INFORMATION:
 E--> 610 (i) APPLICANT: Shuji Hinuma
 E--> 611 Masaki Hosoya

SEQUENCE LISTING

SEQUENCE LISTING

see next page

use (D) before TOPOLOGY at all
 Times
 not (C)

what
 is this?
 looks like a
 format
 error

RAW SEQUENCE LISTING

DATE: 10/18/2002

PATENT APPLICATION: US/09/461,436A

TIME: 13:13:59

Input Set : A:\EP.txt

Output Set: N:\CRF4\10182002\I461436A.raw

E--> 612 Ryo Fujii
 E--> 613 Tetsuya Ohtaki
 E--> 614 Shoji Fukusumi
 E--> 615 u Ala Ile Trp Ala Leu Ser Ala Val Leu Ala Leu
 E--> 616 180 185 190
 618 Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val
 E--> 619 195 200 205
 621 Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu
 E--> 622 210 215 220
 624 Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
 E--> 625 225 230 235 240
 627 Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val
 E--> 628 245 250 255
 630 Val Pro Gly Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
 E--> 631 260 265 270
 633 Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Phe Ala
 E--> 634 275 280 285
 636 Val Cys Trp Leu Pro Leu His Val Phe Asn Leu Leu Arg Asp Leu Asp
 E--> 637 290 295 300
 639 Pro His Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Gln Leu Leu Cys
 E--> 640 305 310 315 320
 642 His Trp Leu Ala Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala
 E--> 643 325 330 335
 645 Trp Leu His Asp Ser Phe Arg Glu Glu Leu Arg Lys Leu Leu Val Ala
 E--> 646 340 345 350
 648 Trp Pro Arg Lys Ile Ala Pro His Gly Gln Asn Met Thr Val Ser Val
 E--> 649 355 360 365
 651 Val Ile
 E--> 652 370

1140 (2) INFORMATION FOR SEQ ID NO: 40:

1142 (i) SEQUENCE CHARACTERISTICS:

1143 (A) LENGTH: 345

1144 (B) TYPE: Nucleic acid

1145 (C) STRANDEDNESS: Double

1146 (D) TOPOLOGY: Linear

1148 (ii) MOLECULE TYPE: cDNA

C--> 1150 (ix) FEATURE:

1151 (C) IDENTIFICATION METHOD: S

1153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

1155 GCTTCCTGGC ACAAGCGTGG AGGTCGCCGT GCTGCTTGGG TAGTGTGTGG AGTCGTGTGG 60

1157 CTGGCTGTGA CAGCCCAGTG CCTGCCACAG GCAGTCTTTG CTGCCACAGG CATCCAGCGC 120

1159 AACC GCACTG TGTGCTACGA CCTGAGCCCA CCCATCCTGT CTACTCGCTA CCTGCCCTAT 180

1161 GGTATGGCCC TCACGGTCAT CGGCTTCTTG CTGCCCTTCA TAGCCTTACT GGCTTGTTAT 240

1163 TGTCGCATGG CCCGCCGCT GTGTCGCCAG GATGGCCCAG CAGGTCTGT GGCCCAAGAG 300

E--> 1165 CGGCGCAGCA AGGCGGCTCG TATGGCTGTG GTGGTGGCAG CTGTC

345 ← insert

E--> 1166 SEQUENCE LISTING

E--> 1169 (1) GENERAL INFORMATION:

E--> 1171 (i) APPLICANT: Shuji Hinuma

E--> 1172 Masaki Hosoya

another format
error

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/461,436A

DATE: 10/18/2002
TIME: 13:13:59

Input Set : A:\EP.txt
Output Set: N:\CRF4\10182002\I461436A.raw

E--> 1173 Ryo Fujii
E--> 1174 Tetsuya Ohtaki
E--> 1175 Shoji Fukusumi
E--> 1176 SEQUENCE LISTING
E--> 1179 (1) GENERAL INFORMATION:
E--> 1181 (i) APPLICANT: Shuji Hinuma
E--> 1182 Masaki Hosoya
E--> 1183 Ryo Fujii
E--> 1184 Tetsuya Ohtaki
E--> 1185 Shoji Fukusumi
E--> 1186 T CGGTGGTGCT GGTGGTCGGC 120
E--> 1188 CTGCCACTGA ACATCTGCGT CATTGCCAG ATCTGCGCAT CCCGCCGGAC CCTGACCCGT 180
E--> 1190 TCCGCTGTGT ACACCCTGAA CCTGGCACTG GCGGACCTGA TGTATGCCTG TTCACTACCC 240
E--> 1192 CTACTTATCT ATAACACGC CAGAGGGGAC CACTGGCCCT TCGGAGACCT CGCCTGCCGC 300
E--> 1194 TTTGTACGCT TCCTCTTCTA TGCCAATCTA CATGGCAGCA TCCTGTTCTT CACCTGCATT 360
E--> 1196 AGCTTCCAGC GCTACCTGGG CATCTGCCAC CCCCTGGCTT CCTGGCACAA GCGTGGAGGT 420
E--> 1198 CGCCGTGCTG CTTGGGTAGT GTGTGGAGTC GTGTGGCTGG CTGTGACAGC CCAGTGCCTG 480
E--> 1200 CCCACGGCAG TCTTTGCTGC CACAGGCATC CAGCGCAACC GCACTGTGTG CTACGACCTG 540
E--> 1202 AGCCCACCCA TCCTGTCTAC TCGCTACCTG CCCTATGGTA TGGCCCTCAC GGTCATCGGC 600
E--> 1204 TTCTTGCTGC CCTTCATAGC CTTACTGGCT TGTATTGTC GCATGGCCCG CCGCCTGTGT 660
E--> 1206 CGCCAGGATG GCCCAGCAGG TCCTGTGGCC CAAGAGCGGC GCAGCAAGGC GGCTCGTATG 720
E--> 1208 GCTGTGGTGG TGGCAGCTGT CTTTGCCATC AGCTTCCTGC CTTTCCACAT CACCAAGACA 780
E--> 1210 GCCTACTTGG CTGTGCGCTC CACGCCCGGT GTCTCTTGCC CTGTGCTGGA GACCTTCGCT 840
E--> 1212 GCTGCCTACA AAGGCACTCG GCCCTTCGCC AGTGTCACAA GTGTTCTGGA CCCCATTCCTC 900
E--> 1214 TTCTACTTCA CACAACAGAA GTTCCGGCGG CAACCCACG ATCTCTTACA GAGGCTCACA 960
E--> 1216 GCCAAGTGGC AGAGGCAGAG AGTC 984

*All next page for
more errors*

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: Other nucleic acid
Synthetic DNA

(ix) ~~(iii)~~ FEATURES:

N is A, G, C, or T

insert → (D) OTHER INFORMATION: ←

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGTGGSCMTS STGGCAACN YCCTG

25

GLOBAL error

do NOT insert
any response

to (ix) FEATURE;
it is a "header"
only.

Explanation of "N,"

etc. go on

(D) OTHER INFORMATION:

line
↓

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/461,436A

DATE: 10/18/2002

TIME: 13:14:00

Input Set : A:\EP.txt

Output Set: N:\CRF4\10182002\I461436A.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
 L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
 L:35 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
 L:72 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
 L:74 M:220 C: Keyword misspelled or invalid format, [(B) REGISTRATION NUMBER:]
 L:74 M:220 C: Keyword misspelled or invalid format, Poss data loss, (B) REGISTRATION NUMBER:
 L:0 M:200 E: Mandatory Header Field missing, [(B) STREET:] of (1)(iv)
 L:512 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
 L:543 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
 L:568 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
 L:595 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:595 M:330 E: (2) Invalid Amino Acid Designator, 3
 L:598 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
 L:598 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:598 M:330 E: (2) Invalid Amino Acid Designator, 3
 M:332 Repeated in SeqNo=26
 L:600 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:600 M:330 E: (2) Invalid Amino Acid Designator, 4
 L:601 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:601 M:330 E: (2) Invalid Amino Acid Designator, 2
 L:602 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:602 M:330 E: (2) Invalid Amino Acid Designator, 2
 L:603 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:603 M:330 E: (2) Invalid Amino Acid Designator, 2
 L:604 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:604 M:330 E: (2) Invalid Amino Acid Designator, 2
 L:605 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:605 M:330 E: (2) Invalid Amino Acid Designator, 2
 L:608 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:608 M:330 E: (2) Invalid Amino Acid Designator, 3
 L:610 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:610 M:330 E: (2) Invalid Amino Acid Designator, 4
 L:611 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:611 M:330 E: (2) Invalid Amino Acid Designator, 2
 L:612 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:612 M:330 E: (2) Invalid Amino Acid Designator, 2
 L:613 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:613 M:330 E: (2) Invalid Amino Acid Designator, 2
 L:614 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:614 M:330 E: (2) Invalid Amino Acid Designator, 2
 L:615 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:615 M:330 E: (2) Invalid Amino Acid Designator, 1
 L:652 M:203 E: No. of Seq. differs, LENGTH:Input:370 Found:339 SEQ:26
 L:661 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
 L:713 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
 L:755 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
 L:782 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
 L:805 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/461,436A

DATE: 10/18/2002

TIME: 13:14:00

Input Set : A:\EP.txt

Output Set: N:\CRF4\10182002\I461436A.raw

L:860 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
 L:899 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
 L:925 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
 L:953 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
 L:986 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
 L:1011 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
 L:1031 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
 L:1069 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
 L:1150 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
 L:1165 M:254 E: No. of Bases conflict, Input:0 Counted:345 SEQ:40
 L:1166 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:1166 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:1169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:1169 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
 L:1169 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:1171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:1171 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:1171 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:1172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:1172 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:1172 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:1173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:1173 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:1173 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:1174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:1174 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:1174 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:1175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:1175 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:1175 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:1176 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:1176 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:1176 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:1179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:1179 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
 L:1179 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:1181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:1181 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:1181 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:1182 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:1182 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:1182 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:1183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:1183 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:1183 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:1184 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:1184 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:1184 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:1185 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/461,436A

DATE: 10/18/2002

TIME: 13:14:00

Input Set : A:\EP.txt

Output Set: N:\CRF4\10182002\I461436A.raw

L:1185 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:1185 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:40
M:254 Repeated in SeqNo=40
L:1216 M:204 E: No. of Bases differ, LENGTH:Input:345 Counted:1230 SEQ:40
L:1225 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:1267 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:1293 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:1324 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:1343 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:1427 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:1475 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:1517 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:1543 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:1585 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:1609 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:1675 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:1713 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:1782 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:1822 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:1903 M:220 C: Keyword misspelled or invalid format, [(ix) FEATURE:]
L:14 M:203 E: No. of Seq. differs, : Input 61, Counted 60